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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/225,502DATE: 01/15/1999
TIME: 12:26:06

Input Set: I225502.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

new format
see p. 5

ENTERED

1 <110> APPLICANT: Moore, et al.
2 <120> TITLE OF INVENTION: Human FK506 Binding Proteins
3 <130> FILE REFERENCE: PF392
4 <140> CURRENT APPLICATION NUMBER: US/09/225,502
5 <141> CURRENT FILING DATE: 1999-01-06
6 <150> EARLIER APPLICATION NUMBER: 60/070,875
7 <151> EARLIER FILING DATE: 1998-01-09
8 <160> NUMBER OF SEQ ID NOS: 8
9 <170> SOFTWARE: PatentIn Ver. 2.0
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13 <213> ORGANISM: Homo sapiens
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20 Met Phe Pro Ala Gly Pro Pro Ser His Ser Leu Leu Arg Leu Pro Leu
21 1 5 10 15
22 ctg cag ttg ctg cta ctg gtg gtg cag gcc gtg ggg agg ggg ctg ggc 156
23 Leu Gln Leu Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly
24 20 25 30
25 cgc gcc agc ccg gcc ggg ggc ccc ctg gaa gat gtg gtc atc gag agg 204
26 Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
27 35 40 45
28 tac cac atc ccc agg gcc tgt ccc cgg gaa gtg cag atg ggg gat ttt 252
29 Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe
30 50 55 60
31 gtg cgc tac cac tac aac ggc act ttt gaa gat ggc aag aag ttt gat 300
32 Val Arg Tyr His Tyr Asn Gly Thr Phe Glu Asp Gly Lys Lys Phe Asp
33 65 70 75 80
34 tca agc tat gat cgc aac acc ttg gtg gcc atc gtg gtg ggt gtg ggg 348
35 Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
36 85 90 95
37 cgc ctc atc act ggc atg gac cga ggc ctc atg ggc atg tgt gtc aac 396
38 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
39 100 105 110
40 gag cgg cga cgc ctc att gtg cct ccc cac ctg ggc tat ggg agc atc 444
41 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
42 115 120 125
43 ggc ctg gcg ggg ctc att cca ccg gat gcc acc ctc tac ttc gat gtg 492
44 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val

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49      ttg ctg cgc ccg ccc cac tgc ccc cgc atg gtc cag gac ggc gac ttt 588
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52      gtc cgc tac cac tac aat ggc acc ctg ctg gac ggc acc tcc ttc gac 636
53      Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
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55      acc agc tac agt aag ggc ggc act tat gac acc tac gtc ggc tct ggt 684
56      Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
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62      Gln Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
63          225          230          235          240
64      ggc tat ggt gag ggt ggg caa gga cac aag ggg aaa ttc cgc aga aga 828
65      Gly Tyr Gly Glu Gly Gly Gln Gly His Lys Gly Lys Phe Arg Arg Arg
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91          20          25          30
92      Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
93          35          40          45
94      Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe

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98 Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
99          85          90          95
100 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
101          100          105          110
102 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
103          115          120          125
104 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
105          130          135          140
106 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
107          145          150          155          160
108 Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
109          165          170          175
110 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
111          180          185          190
112 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
113          195          200          205
114 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
115          210          215          220
116 Gln Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
117          225          230          235          240
118 Gly Tyr Gly Glu Gly Gly Gln Gly His Lys Gly Lys Phe Arg Arg Arg
119          245          250          255
120 Gly Lys Asn Gln Ala Ser Thr Tyr Ser Cys Ser Gly Cys Ile Leu His
121          260          265          270
122 Glu Gly Ile Gln Pro Arg Thr Gln Gly Gly Met Lys Ser Thr Leu Gly
123          275          280          285
124 Ala Thr Lys Lys Gly Cys Phe Gly Arg Ala Trp Trp Leu Thr Leu Val
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138       1          5          10          15
139 gtg agc aca ttg ctg cgc ccg ccc cac tgc ccc cgc atg gtc cag gac 97
140 Val Ser Thr Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp
141          20          25          30
142 ggc gac ttt gtc cgc tac cac tac aat ggc acc ctg ctg gac ggc acc 145
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144          35          40          45

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149	Gly Ser Gly Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met	
150	65 70 75 80	
151	tgt cct gga gag aga agg aag att atc atc cct cca ttc ctg gcc tat	289
152	Cys Pro Gly Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr	
153	85 90 95	
154	ggc gag aaa ggc tat ggg aca gtg atc ccc cca cag gcc tcg ctg gtc	337
155	Gly Glu Lys Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala Ser Leu Val	
156	100 105 110	
157	ttt cac gtc ctc ctg att gac gtg cac aac ccg aag gac gct gtc cag	385
158	Phe His Val Leu Leu Ile Asp Val His Asn Pro Lys Asp Ala Val Gln	
159	115 120 125	
160	cta gag acg ctg gag ctc ccc ccc ggc tgt gtc cgc aga gcc ggg gcc	433
161	Leu Glu Thr Leu Glu Leu Pro Pro Gly Cys Val Arg Arg Ala Gly Ala	
162	130 135 140	
163	ggg gac ttc atg cgc tac cac tac aat ggc tcc ttg atg gac ggc acc	481
164	Gly Asp Phe Met Arg Tyr His Tyr Asn Gly Ser Leu Met Asp Gly Thr	
165	145 150 155 160	
166	ctc ttc gat tcc agc tac tcc cac aac cac acc tac aat acc tat atc	529
167	Leu Phe Asp Ser Ser Tyr Ser His Asn His Thr Tyr Asn Thr Tyr Ile	
168	165 170 175	
169	ggg cag ggt tac atc atc ccc ggg atg gac cag ggg ctg cag ggt gcc	577
170	Gly Gln Gly Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu Gln Gly Ala	
171	180 185 190	
172	tgc atg ggg gaa cgc cgg aga att acc atc ccc ccg cac ctc gcc tat	625
173	Cys Met Gly Glu Arg Arg Arg Ile Thr Ile Pro Pro His Leu Ala Tyr	
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175	ggg gag aat gga act gga gac aag atc cct ggc tct gcc gtg cta atc	673
176	Gly Glu Asn Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala Val Leu Ile	
177	210 215 220	
178	ttc aac gtc cat gtc att gac ttc cac aac cct gcg gat gtg gtg gaa	721
179	Phe Asn Val His Val Ile Asp Phe His Asn Pro Ala Asp Val Val Glu	
180	225 230 235 240	
181	atc agg aca ctg tcc cgg cca tct gag acc tgc aat gag acc acc aag	769
182	Ile Arg Thr Leu Ser Arg Pro Ser Glu Thr Cys Asn Glu Thr Thr Lys	
183	245 250 255	
184	ctt ggg gac ttt gtt cga tac cat tac aac tgt tct ttg ctg gac ggc	817
185	Leu Gly Asp Phe Val Arg Tyr His Tyr Asn Cys Ser Leu Leu Asp Gly	
186	260 265 270	
187	acc cag ctg ttc acc tcg cat gac tac ggg gcc ccc cag gag gcg act	865
188	Thr Gln Leu Phe Thr Ser His Asp Tyr Gly Ala Pro Gln Glu Ala Thr	
189	275 280 285	
190	ctc ggg gcc aac aag gtg atc gaa ggc ctg gac acg ggc ctg cag ggc	913
191	Leu Gly Ala Asn Lys Val Ile Glu Gly Leu Asp Thr Gly Leu Gln Gly	
192	290 295 300	
193	atg tgt gtg gga gag agg cgg cag ctc atc gtg ccc ccg cac ctg gcc	961
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TIME: 12:26:06

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201      340      345      350
202      ctg ttt gtg tgg cac aag gac cct cct gcc aac ctg ttt gaa gac ata 1105
203      Leu Phe Val Trp His Lys Asp Pro Pro Ala Asn Leu Phe Glu Asp Ile
204      355      360      365
205      gac ctc aac aag gat ggc gag gtc cct ccg gag gag ttc tcc acc ttc 1153
206      Asp Leu Asn Lys Asp Gly Glu Val Pro Pro Glu Glu Phe Ser Thr Phe
207      370      375      380
208      atc aag gct caa gtg agt gag ggc aaa gga cgc ctc atg cct ggg cag 1201
209      Ile Lys Ala Gln Val Ser Glu Gly Lys Gly Arg Leu Met Pro Gly Gln
210      385      390      395      400
211      gac cct gag aaa acc ata gga gac atg ttc cag aac cag gac cgc aac 1249
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214      cag gac ggc aag atc aca gtc gac gag ctc aag ctg aag tca gat gag 1297
215      Gln Asp Gly Lys Ile Thr Val Asp Glu Leu Lys Leu Lys Ser Asp Glu
216      420      425      430
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224      cctgtggagc ctgggggttg atagggccat ggctgtgccc ccaccatacc tcccctccac 1644
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242      20 25 30
243      Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr
244      35 40 45

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I225502.RAW

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505	W "N" or "Xaa" used: Feature required	tattcccagc agcctgtgca aattctgatg atggcccc
506	W "N" or "Xaa" used: Feature required	acatcawgct tttccagctc atcacacccc gcccant
507	W "N" or "Xaa" used: Feature required	atnanttga ggntaaaaga gccttttgga cagaaaac
508	W "N" or "Xaa" used: Feature required	gaccacaaat agagaatttg attcgtcatt tgccacan
509	W "N" or "Xaa" used: Feature required	tttccttnan ananatttna ntttttctg gaggcaga
569	W "N" or "Xaa" used: Feature required	Gly Leu Leu Gly Val Cys Ile Gly Glu Lys A
587	W "N" or "Xaa" used: Feature required	Ala Val Leu Val Phe Asp Ile Glu Xaa Leu G